

FIG. 1

GENETIC MARKERS, STSs,
 AND RECOMBINANTS

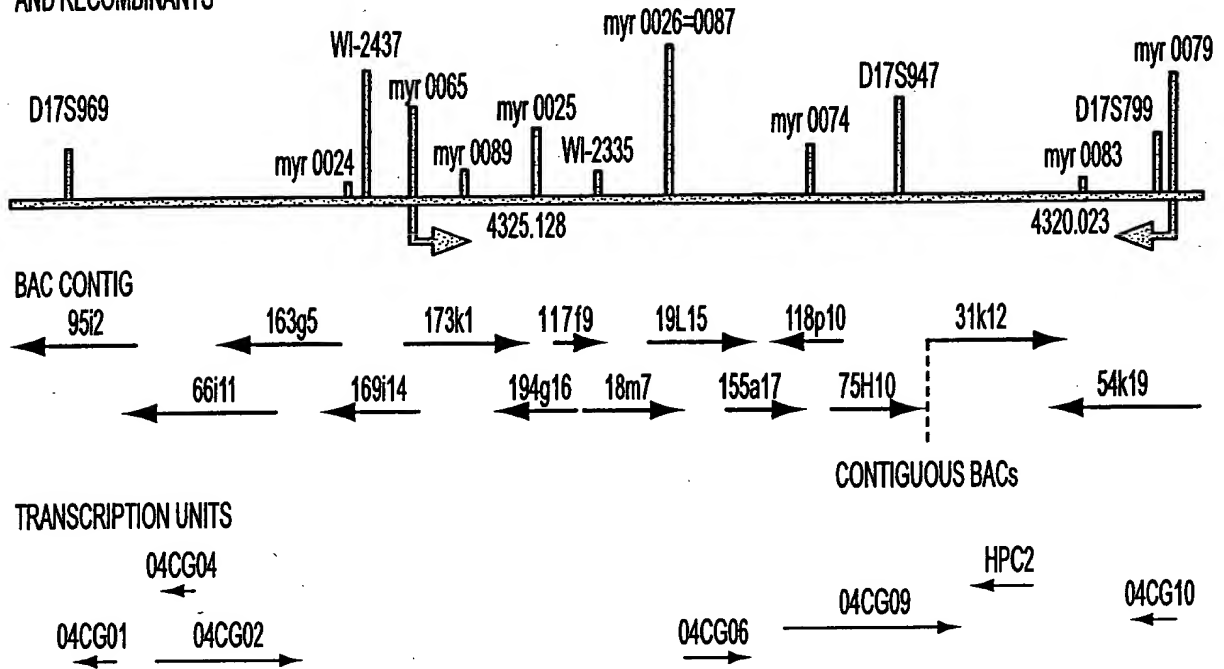


FIG. 2A

BAC 31k12 WITH 2 EXONS OF 04CG09 AND THE HPC2 TRANSCRIPTION UNIT

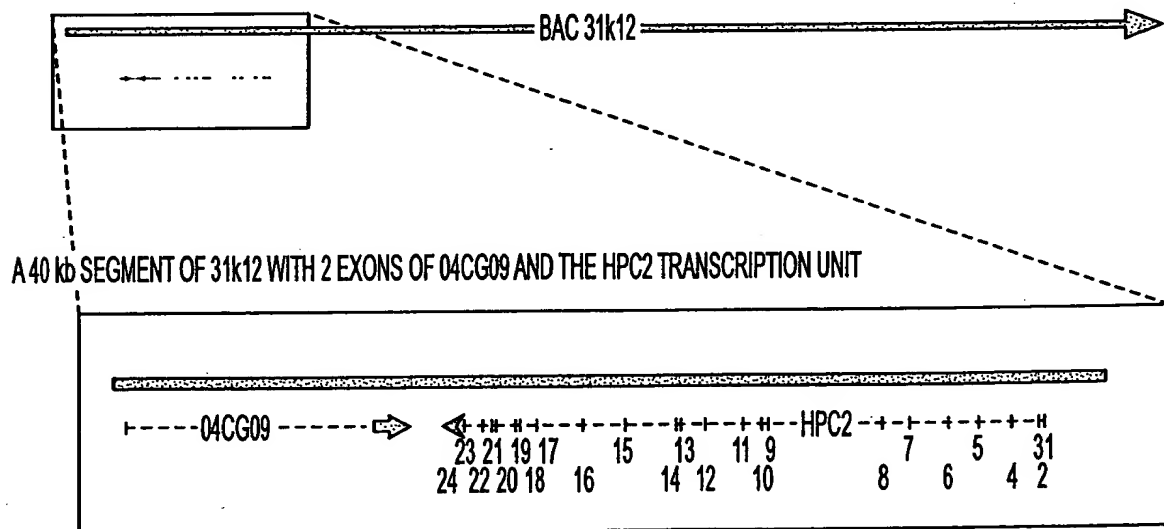


FIG. 2B

FOOTNOTES 28988660

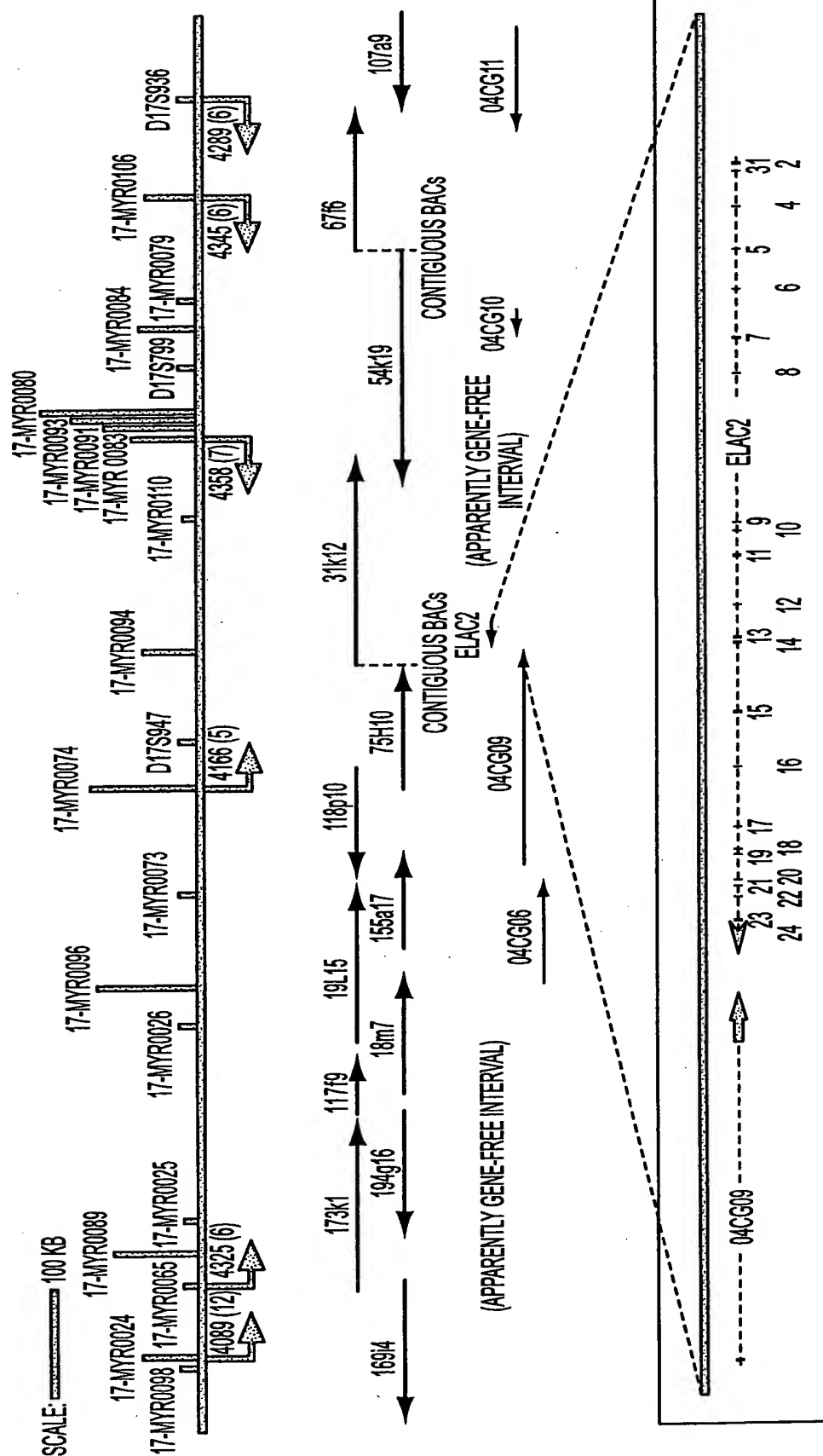


FIG. 3

09988687-112001

Hs.HPC2.exon1	cgcgggcgtaggtgaccggcggttttctcagttttggtggagacgggagc
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	tggcgggcgtaggggtctggctgccttgtcagcctggtgtggtcggtgc
Mm.HPC2.exon1.pep	----- ----- ----- ----- -----
	1 11 21 31 41
Hs.HPC2.exon1	ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTC
Hs.HPC2.exon1.pep	M--W--A--L--C--S--L--L--R--S--A--A--G--R--T--M--S--
Mm.HPC2.exon2	ATGTGGGCGCTCCGCTCACTGTTGCGTCCCCTTGGCCTGCGACCATGTC
Mm.HPC2.exon1.pep	M--W--A--L--R--S--L--L--R--P--L--G--L--R--T--M--S--
	----- ----- ----- ----- -----
	51 61 71 81 91
Hs.HPC2.exon1	GCAGGGACGCACCATATCGCAGGCACCCGCCCGCCGCGAGCGGCCGCGCA
Hs.HPC2.exon1.pep	-Q--G--R--T--I--S--Q--A--P--A--R--R--E--R--P--R--K
Mm.HPC2.exon2	GCAGGGT-----TCGGCTCGTCGGCCCGCGGCCACCCA
Mm.HPC2.exon1.pep	-Q--G-----S--A--R--R--P--R--P--P--K
	----- ----- ----- ----- -----
	101 111 121 131 141
Hs.HPC2.exon1	AGGACCCGCTGCGGCACCTGCGCACGCGAGAGAAGCGCGGACCGTCGGGG
Hs.HPC2.exon1.pep	--D--P--L--R--H--L--R--T--R--E--K--R--G--P--S--G--
Mm.HPC2.exon2	AAGACCCACTGCGACACCTGCGTACGCGGAGAGAAGCGCGGCCCGGGT---
Mm.HPC2.exon1.pep	--D--P--L--R--H--L--R--T--R--E--K--R--G--P--G----
	----- ----- ----- ----- -----
	151 161 171 181 191
Hs.HPC2.exon1	TGCTCCGGCGGGCCAAACACCGTGCTACCTGCAGGTGGTGGCAGCGGGTAG
Hs.HPC2.exon1.pep	C--S--G--G--P--N--T--V--Y--L--Q--V--V--A--A--G--S--
Mm.HPC2.exon2	---CCCGGGGGCCCGAACACCGTGCTACCTGCAGGTGGTGGCGGGCGGGCGG
Mm.HPC2.exon1.pep	---P--G--G--P--N--T--V--Y--L--Q--V--V--A--A--G--G--
	----- ----- ----- ----- -----
	201 211 221 231 241
Hs.HPC2.exon1	CCGGGACTCGGGCGCGCGCTCTACGTCTTCTCCGAGTTCAACCGgtcag
Hs.HPC2.exon1.pep	-R--D--S--G--A--A--L--Y--V--F--S--E--F--N
Mm.HPC2.exon2	CCGGGACGCGGGGGCTGCTCTATGTCTTCTCGGAATACAACAGgtcag
Mm.HPC2.exon1.pep	-R--D--A--G--A--A--L--Y--V--F--S--E--Y--N
	----- ----- ----- ----- -----
	251 261 271 281 291
Hs.HPC2.exon1	tcaacgagccacgccccgtcccgtggtccctcagtgcgccgcagcctct
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	agtgggcccagagccctgggggattggccccagcgccacgtgctcgggag
Mm.HPC2.exon1.pep	----- ----- ----- ----- -----
	301 311 321 331 341

FIG. 4

FIG. 5A

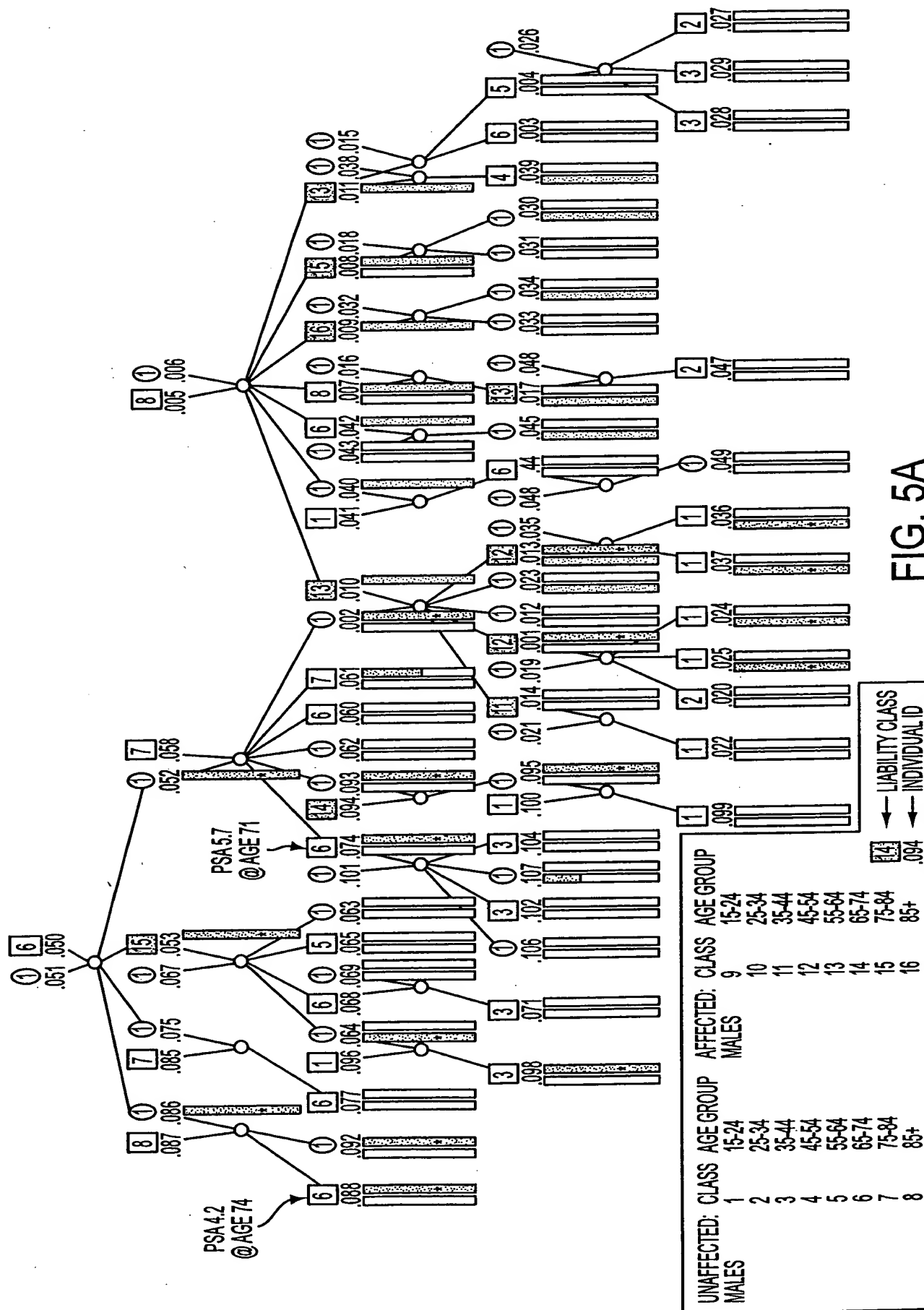


FIG. 5A

FOOT-2898660

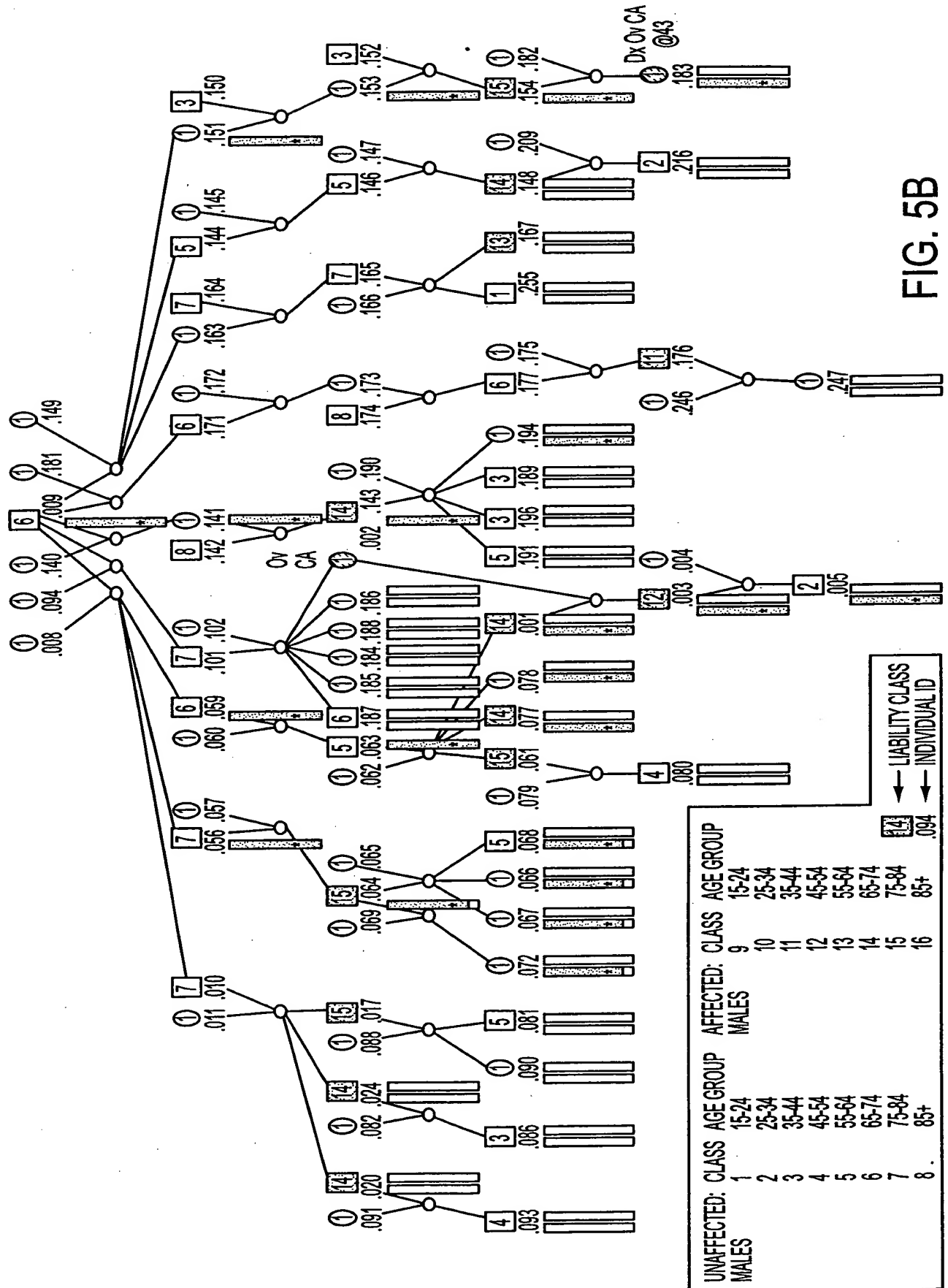


FIG. 5B

FOOZTT 28988660

(HSA) ELAC2	1	MWALCSLLRSAAGRMTNSQRTISQAPARPRPRKXDPHRLTRKRGPSGSGGPNVYLQWVA
(MMU) Elac2	1	MWALRSLLRPLGLRTMSQG.....SARQPRPSKDPHRLTRTRKRGPGGGPNVYLQWVA
(CEL) CE16965	1	MXMLRFGIKVSRHLISSTCLFKDNNBELLESIKERIAARRILOHSSSHLKAREVNASISNLRQSMAAVQKQKAAHEPPANS·IVNIPSQVSTIEVLG
(ATH) gi6850339	1	MENNEATNGSKSSSSNSPVFNKRAAGFDITDKKRNLERKSQK·LNPTNTIAYAQILG
(SCE) YKR079C	1	MPTFIPITTH
(HSA) ELAC2	65	AGSRDGAALYVFSEFNR·YLPNCGEGVQRLNQEHKLKVARLDNIFLT·RMHWSNVGSGSMILTKETGLPK·CVLSGPPQLKXVL·EAINIF.....
(MMU) Elac2	57	AGGRDACAALYVFSEYNR·YLPNCGEGVQRLNQEHKLKVARLDNIFLT·RMHWSNVGSGCMILTKETGLPK·CVLSGPPQLKXVL·EAINIF.....
(CEL) CE16965	100	N·GTGLLRACFILTPLKT·YMPNCPENACFLWQLRIRSSVVDLFIIT·SANWDNIAGTSSILLIS·KESNALS·TRLHGAMNKHFL·ECIRPFQDSD
(ATH) gi6850339	58	TGMDTDTSSNLLFPDKQRIIPNAGGLQRFCTEHKIKLSKIDHVLIS·RVCSETAGGUPGLLLITAGIGBEGLSVNWGSPDLNIVL·DAMKSEIPRA
(SCE) YKR079C	10	PTSDTKHPPLLWQSAHGXVFEGKIFEGSQRSITENKIRISKLDIFLTGELNWSDIGPILPMILITADQGXSN·LVHLYGNDILNIVSTWRYVVRFR
(HSA) ELAC2	155SGPLK·GIELAVR·.....PHSAPEYDETMVYQIPIHSQRGRGHQWPQSPRPLSRLSPESSDSSESNENBHLPL·
(MMU) Elac2	147SGPLK·GIELAVR·.....PHSAPEYDETMVYQVPIHSERRCGKQOPSQSPRTSPNRLSPKQSSDGSSEN·GQCPE
(CEL) CE16965	193YGSCKY·PSQVER·.....PTMENYEDAGLWYIP·.....LSP·PLNIGSNNEKS·.....
(ATH) gi6850339	156	AMVHTRSGPSSPDPIVLVNDDEVKISAIL·.....LXP·CHSBEEDSGNKSQD·.....
(SCE) YKR079C	108GIDENDHMKDXYKDKLIAVKSFNKNGGDRLEMPDSFQKGVLSIVA·.....KMPPKHAPTDTRYDPSDDPHLN·.....
(HSA) ELAC2	226	·HGVSORRGV·RDSLSLVAVATCKHLKRGNFLVLKAKENGHPVGTAAIAPITIAAVKDGKSTT·HEGEHILABEELCTP·.....PDPGAARFWVVECP·DESF
(MMU) Elac2	219	DSSAGANRKANGRPDSLVAATVCKHLKRGNFLVLKAKELGIPVGTAAIAPITIAAVKDGKSTT·YEGREHIAABEELCTP·.....PDPLGLVEIIVVECP·DEGF
(CEL) CE16965	238	·KNV·KVNVDIAHLEMKBAARRIDTWKLMELKVP·K·GP·LIGKLSGEAVTLPDGRTHQPDQVFSDDKVEGDKPLL·LWTECTTETH·
(ATH) gi6850339	203	·LSVVVVCCELPEILGKFDLEKAKK·VGVKVPKPYSRLOSSES VKS·DERDITVHPSDWMGP·SILPGPIVLLVDCPTESHA
(SCE) YKR079C	181	·VELPDLDAVVESTNVEISFSPVRGKFKVEAIKLGVP·K·GP·LEAFLTKGHTLDNGIIVTPPEQVLENER·HFAKVLILDIP·DDLY
(HSA) ELAC2	317	IQPICENATFORQCKADAPVAL·VHMAPASVLVDSNQW·MERFGPDQ·HLVIMENCASVNL·RSHKIQTQLMLIHPDIEPLL·.....
(MMU) Elac2	313	ILPICENDTFKRYQAEADAPVAL·AVHIAPEBVLSIDSRNQW·MERFGPDQ·HLIIMENCPSVNL·RSHKIQTQLSLIHPDIEPLL·.....
(CEL) CE16965	322	VKALIDSSSIQPFNGEKQLDY·VHISDDAVINTPTVRHL·MEKLNPSITHELLINGGNPVIAVESVYKHTRLRSIAPSLFPAL·.....
(ATH) gi6850339	280	ABIEFLSKLSIESYSSPDEQTIGAKFVNCIHLSPSSVTSPTVQSW·MKKEHL·TQ·HILAGHORFLPLLIIVSQHT·VRKNWAPILKASSRIAA
(SCE) YKR079C	266	LNAAFEVK·FKDYDCA·ELGMVYVFLGDEVTINDNLFAPIDIEKNVYGVNHH·MISENKISINTISFPGSALTITLKALQV·NNYMLPKTDRVFSKDF

FIG. 6A-1

TABLE 2838666

(HSA) ELAC2	401	...TSPRCKKEGPTLSVPMVQGECLLKYLPRPRRQR...	...DAITCNPEEFIVEM...	...QLPNFQSQVQYRRSAQDG...
(MMU) Elac2	397	...TSFYSKEEGSTISVPTVRGECLLKYLPRPKRWR...	...DTLDCNDEPIABAL...	...ELPSFQSEVEYRKNVQEN...
(CEL) CE16965	407	...HPIDWSGIITONEELSORDDQFIRV-APMQRVWR...	...RGA...	...SPPEPIVNNLLAAEPPLSDKAK.ELIKEYOK...
(ATH) gi6850339	374	RLNYLCPOFFPAPGFWPSQLTDSHIDPPSNKP-NLRPVAIRGIDRSCIPAPLTSSEVVDLLSEIPEIKDKSEIKQFNNKQHNKTIIEKLWLSECNT		
(SCE) YKR079C	362	YDRFDTPLSRGTSMKCSQEEPLNTLLEKDNHIFSQNKTVTPPEPRMNEBPMKCNINGEVADFSWQEIPEE-HVKPPL-EPPLADVD-TVINNQLHVDN...		
				1641 insg
(HSA) ELAC2	471	...PAPAEKRSQYPEIIF.LGTGSAIPMKIRNVSAIWNISP...	...DTSLLDCCGEGTGGQLCRHYGQ...	...VDRWLGTLAANFVSHLHADHHTGLPSI
(MMU) Elac2	467	...PAPAEKRSQYPEIIF.LGTGSAIPMEIRNVSTLWNLSL...	...DKSWLLDCCGEGTGGQLCRHYGQ...	...IDRWLCSLTAVFVSHLHADHHTGLLNI
(CEL) CE16965	475	...LEKENKMDCEFPKLTFFGTSSAVPSKYRNVTC-VLVREASB...	...NSAILIDVCEGTYGOMRAVFGEDGCKQLLVNLCNVLITHAQDHMNGLYTI	
(ATH) gi6850339	473	VLPNCLEKIRRDDMEIVILGTGSSQPSKYRNVSAIPFDLFS...	...RGSLLDCCGEGTGGQLCRHYGLDGADENRKLRCIWIWISHIHADHHTGLARI	
(SCE) YKR079C	456	FNNSAEKKHVEIIT.LGTGSAIPSKYRNVVSTLWKVPFTDADGNTINRNIMLDACENTLGTIHRMESQLAVKSHQDLKMEYLSHLHADHHTGLISV		
(HSA) ELAC1	1	MSMDVTF.LGTGAAYPSPTGASAVTIRCE...	...GECWLFDCGEGTQTQD...	...MKSQKAGRIITKLIITITHLHGCHPFGLPGL
(Es c) elac	1	MKRDELMEIIF.LGTSAVPTRTNNTA-TILNLQHPF...	...QSGLWLFDCGEGTQHQL...	...LHTAPNFKGLDKHIFISHLHGCHLFGLPGL
(Syn_sp) gi2500943	1	MEITP.LGTSSGVPTRNNVSS-TIALRLPQ...	...RAELWLFDCGEGTQHOF...	...LRSEVMESQLTRUFTITHLHGCHLFGLMGL
(Me t) gi2622965	1	MNEVTF.LGTSSAVPSKNNETS-TIALRIP...	...GEIIFLDCGEGTQROM...	...ALAGISDNKUTRIFTITHLHGCHLFGIPGM

FIG. 6A-2

FIG. 6B-1

(HSA) ELAC2	559	LLQPERALASLGKPLHPLVLPNQLKAWLQQYHNQCQEVLLHISMIPAKCLQEGABISSPAVERLISSLRTC
(MMU) Elac2	555	LLQREHALASLGKPPFLLVWAPTLQRAWLQQYHNHCQELHHSVMIAPAKCLQGAEVSNITLERLISLLETCT
(CEL) CE16965	565	ILARRKEAFESLGAPEPLVLVCRNWLKPMKTYISCTENIEHLLEIVDISRYPLTPPGSPGGPKRPRLPSPHLPSPDLQDM
(ATH) gi6850339	564	LAL..RSKLLKGVTHEPVIWGPRLKRRELDAYQRLLEDLMEFLDCRSTATSWASLESGBAEGSLFTQ..GSPMQSVFKRSDISMNSSVLLC..LK
(SCB) YKR079C	554	L..NEWYKYNKDDETSIVYVWTPQVYHKFNEML..VLENKEILKRIKIYISCEHFINDSFVRMOTQSVPLABFNEILKENSNOESNRKLELRDSSRYDVD
(HSA) ELAC1	75	LC..TISLQSGSMVSKQPIEIIYGPVGLRDFIWRMTWELSHTELVFHYV..HELVPADQCPAEELKEFAHVNRAVS
(Es c) elac	83	L.....CSRNSGIIQLTIYGPQCIREFMETAL
(Syn sp) gi2500943	75	L.....ASSGLAGSGQIEIYGPGLGDIKEACC
(Me t) gi2622965	74	L.....QSMGPRGREZPDIIYGPGLHELHECTM
(HSA) ELAC2	633DUEEFQTCIVRHCKH..AFGCALVHTSGWKWVYSGDTMP..CBAL
(MMU) Elac2	629DUEEFQTCIVRHCKH..AFGCALVHSSGWKWVYSGDTMP..CBAL
(CEL) CE16965	650	SSSPDKKAWKLDLKAQVHHTRMANGFVMRVAGKRIVPSGDTMP..CDLL
(ATH) gi6850339	657	NLKKVLSBIGLNDLISFPVHCPQAYGWVIXMAERVNSVGEQILGKWKWVYSGDSRP..CPBT
(SCB) YKR079C	651	LIRQVYEDLSIEYFQTCRAIHCDW..ATNSNHTFRMDENNEHNTFKVSYSGDTRPNIEKF
(HSA) ELAC1	163	NSYLLFDDEQV..WKAFRTHRIIPSPGFSVVEKKRPGKLNQKLDLGVPPGPAYGKLNKNGISVVLNENGVTISPDVLKAPIVGRKICILGDCSGVVG
(Es c) elac	130	..GEIIDDGLRK..VTAYDIEHPLECYGRIEEDHKPGALNAQALKAAGVPPGLFQELKAGKTTITLEDGRQINGADYLAAPVPGKALAIFFDTCDECDA
(Syn sp) gi2500943	122	N..GLIYEDKDFQ..VHCGLLKHRIPAGVRVVEEKORPGRNVEQABALGIPFGPIYGQLKQKTVTLEDGRRIRGQDLCEPPEPGRKFWYCTDTVFCEBA
(Me t) gi2622965	121	G..TVV..EEDDYR..VTSAPASHSVFNLANCFEBEKKRPR..FLREKAIAGLKPDAFGKLRHGIPVRVGRIINPEEVLGSPRKGVKVCYSGDTMP..CESV

FIG. 6B-1

FIG. 6B-2

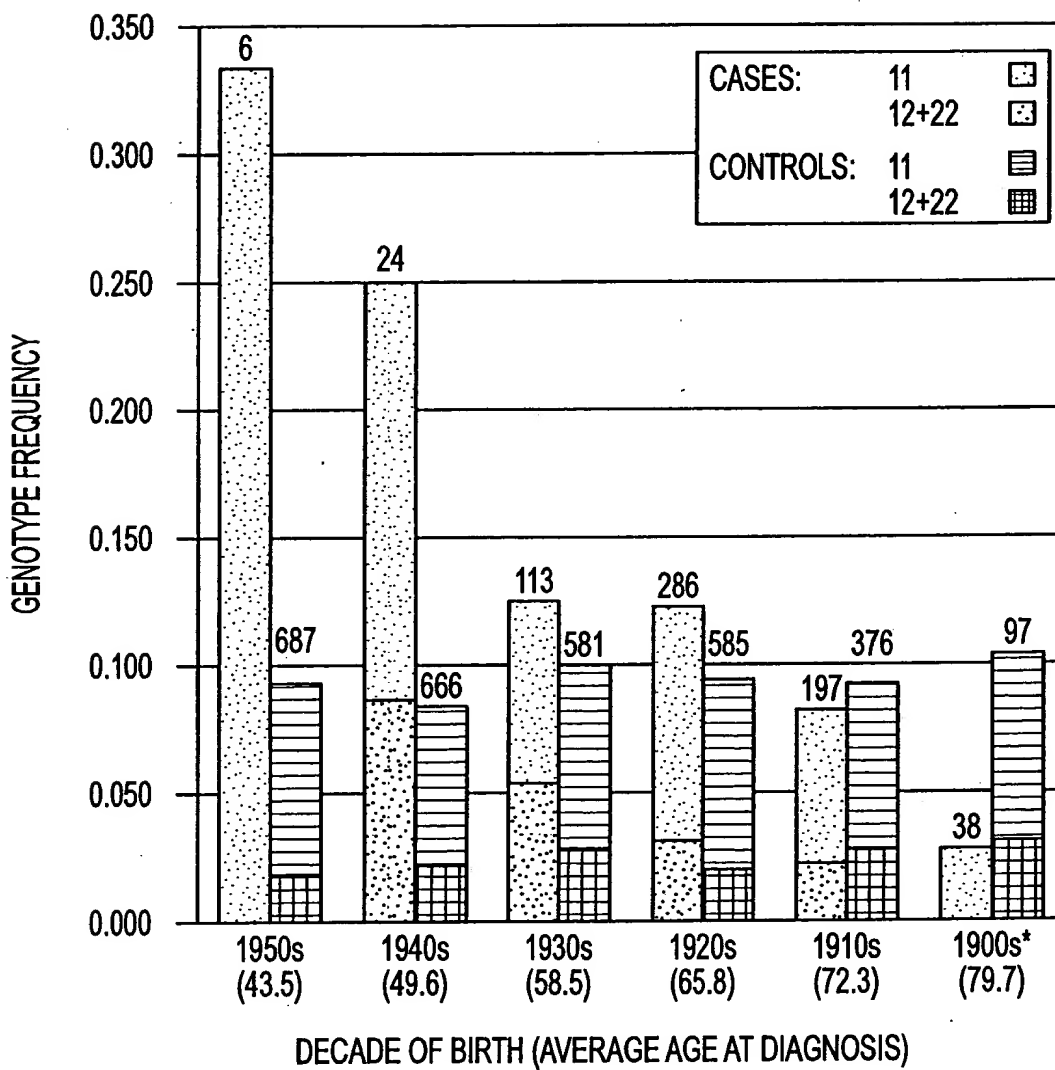


FIG. 7

	OBSERVED	
	CASES	CONTROLS
00, 01, 02	372	139
11, 12, 22	57 (13.3%)	9 (6.1%)

00, 01, 11	387	143
02, 12, 22	42 (9.8%)	5 (3.4%)

00, 01	347	137
02, 11, 12, 22	82 (19.1%)	11 (7.4%)

1920s - 1950s CASES VS. PEDIGREE UNAFFECTEDS

00, 01, 02	372	2151
11, 12, 22	57 (13.3%)	220 (9.3%)

00, 01, 02	372	2151
11	40 (9.3%)	170 (7.2%)
12, 22	17 (4.0%)	50 (2.1%)

ODDS RATIO 11	1.4
ODDS RATIO 12,22	2.0
P-VALUE	0.017
TREND STATISTIC	8.09
P-VALUE	0.004

FIG. 8

FIG. 9-1

CPSF73 family	
(HSA) CPSF73	1 MSAPAEESDQILRPLGAGQEVGRSCILLEFKGRKIMLDCGIIHPC · LEGWDALPY · IDLIDPAEIDLLISHFHLDCGALPWFLOXT
(ATH) gi6751699	1 MASSSTSLKRRQPISTRDGDQIIVTPLGAGSEVGRSCVMSFKGNILDCGIIHPC · YSGMAALPY · FDEIDPSSIDVLLITRPHIDHAASLPYRJEKT
(SCE) YSH1	1 MERTNTTTFKPFSLGGSNEVGRSCHILQYKGTWMDAGIHPA · YQGLASLP · YDEFDLSKWDILLISHFHLDCGALPYPYVWORT
(Syn sp) gi2496795	1 MTGSVPTQGAFAFANISLPGVGRPD · GGICLHLGCPYRILDCGLEB · · · · · DPCTVDLVCCSHARDHIGLWQFHQOP
(Me_t) gi2622312	161 ILQQLGNRIHQKPKVDND · WARDTA · NGGPREVGRSCLYLQTPNSRVLLDCGVNAGDDKNSVPYLNVPFETLDSADAVIITHAHLDHSGELPYL · YHY
PS02 family	
(HSA) ha3611	651 KRSDHLIN · TESEAVNLSKVKETKSA · HGLQGRNKKIPSSNVGGRKATCPFKAKIPGTGTVDAPQVGVVEGCTANFLTRFHSDEHVAGLSKHPTFP
(ATH) gi2979557	350 TANKLITRFPFGQATGCTKIRTAAPKPAEKSPSDSSRAVRNRNGNKGKVPHPHMCIPGTTPRVDAFKYLTRD · CCHMFLTRFHLDHVQGLTKSPSHG
(SCE) PS02	165 HCDTCIGSDPSNMGTGPKNIRSFISNPSPAKTKRDIATSKKPRVKLVLPSPKIIKFNNGHEIVVDGPNYKASETISQVFLSHFHSDEHYIGLKKSMMNP
ELAC2 family	
(HSA) ELAC2	481 · · · · · PEIIFLGTGSAIPKIRINVSATLVNISP · · · · · DTSLLDGEGEGTGGOL · CRHYGDQ · VDRVLGTDAVENSVSHADHHTGLPSILQOR
(ATH) gi6850339	485 · · · · · MEIVILGTGSSQSKYRNVSALFIDFS · · · · · RGSLLDGCGETLGGOL · KRRVGLDGADEAVRKLRCIMISHHADHHTGLARILAIR
(SCE) YKR079C	466 · · · · · VEIITLGTGSAIPKIRINVSATLVNISP · · · · · NRNIMLDAGENTLGTI · HRMFSQALAVKSIPODLKMINVLSHSHADHHTGLISVLNEN
CPSF73 family	
(HSA) CPSF73	148 · · · · · GIKFWCYHAGHVLGAMFMIRIA · · · · · GVKLLVTCGDFS · · · · · RQEDRHLMAAEIPNIK · PDILHIESTGTHI · HEKREEREARFCNTVH
(ATH) gi6751699	158 · · · · · GIKFWCYHAGHVLGAMFMIRIA · · · · · GVRILYTCGYS · · · · · REEDRHLMAAEIPNIK · PDILHIESTGTHI · HEKREEREARFCNTVH
(SCE) YSH1	153 · · · · · GIKFTAFHAGHVLGAMFMIRIA · · · · · GVRILYTCGYS · · · · · REEDRHLMAAEIPNIK · PDILHIESTGTHI · HEKREEREARFCNTVH
(Syn sp) gi2496795	125 · · · · · GUTVELLPAGHLPAGHLLILEYHNG · · · · · DRLRVINTGDIYCLSHLQVLDGALTPLRGLK · PDVILLEGHGNRR · LPHRRQERQFQIAIE
(Me_t) gi2622312	319 · · · · · DRLTLHAGHILGSMHHTIG · · · · · DGQNMVYTCGPK · · · · · YEQSRLLLEAANRPP · IETAVRSTYGGHEDVQPSNRRAEKLVTIY
PS02 family	
(HSA) ha3611	783 · · · · · GVKWLLDANHCPCGAVILFVLP · · · · · NGVILHTGDFRADPSNERSLLADOK · · · · · VHMVLDITTCSPPEYTFPSQOEVRFAINTAF
(ATH) gi2979557	484 · · · · · GUDVTCFDANHCPCGAVILFVLP · · · · · NGVILHTGDFRADPSNERSLLADOK · · · · · VHMVLDITTCSPPEYTFPSQOEVRFAINTAF
(SCE) PS02	308 · · · · · TISWVTLNHCPCGAVILFVLP · · · · · NSVDKPIRQILHTGDFRADPSNERSLLADOK · · · · · VHMVLDITTCSPPEYTFPSQOEVRFAINTAF

FIG. 9-1

FIG. 9-2

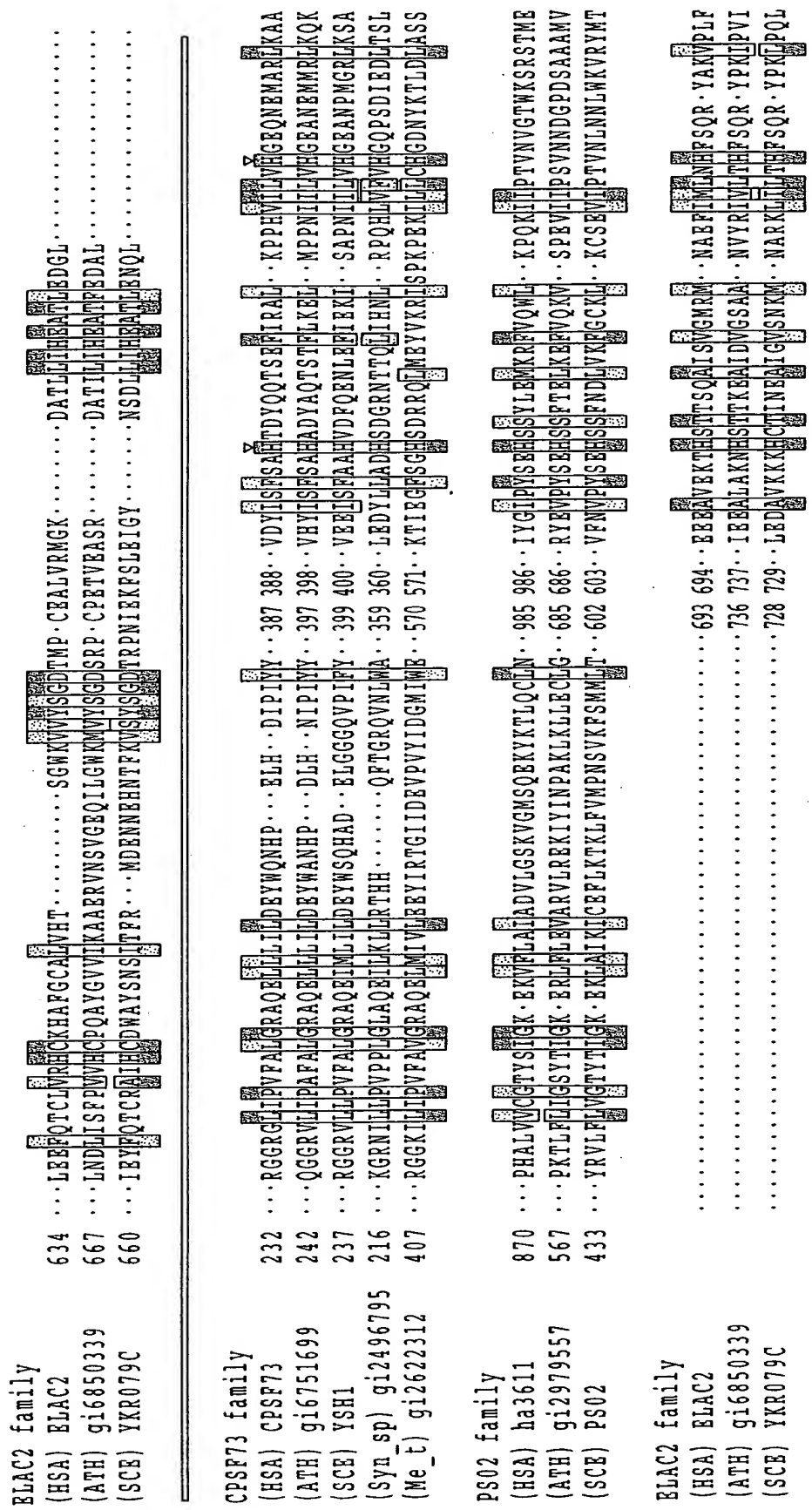


FIG. 9-2

TABLE 28333660

	(HSA) ELAC2			(MMU) Elac2			(CEL) CE16965			(ATH) gi6850339			(SCE) YKR079C		
	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP
(HSA) ELAC2	100.0	100.0	0.0	-	-	-	-	-	-	-	-	-	-	-	-
(MMU) Elac2	81.6	88.0	1.8	100.0	100.0	0.0	-	-	-	-	-	-	-	-	-
(CEL) CE16965	24.2	43.0	14.0	24.6	44.0	15.7	100.0	100.0	0.0	-	-	-	-	-	-
(ATH) gi6850339	25.6	47.0	23.5	25.4	46.0	25.0	21.0	44.0	21.1	100.0	100.0	0.0	-	-	-
(SCE) YKR079C	21.8	41.0	20.8	21.7	43.0	21.4	18.2	43.0	21.4	21.8	41.0	16.3	100.0	100.0	0.0

FIG. 10

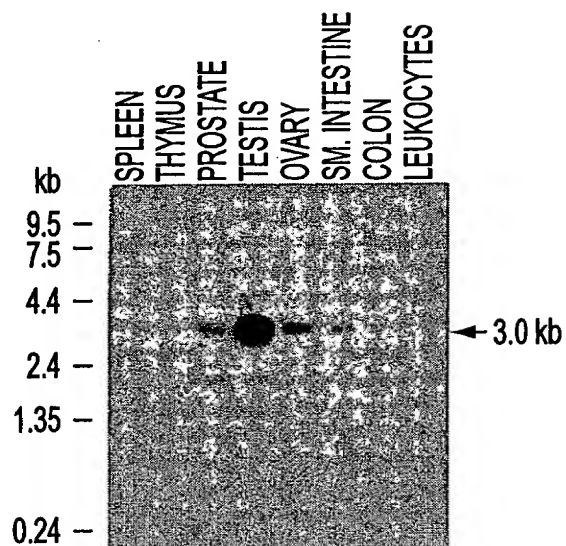
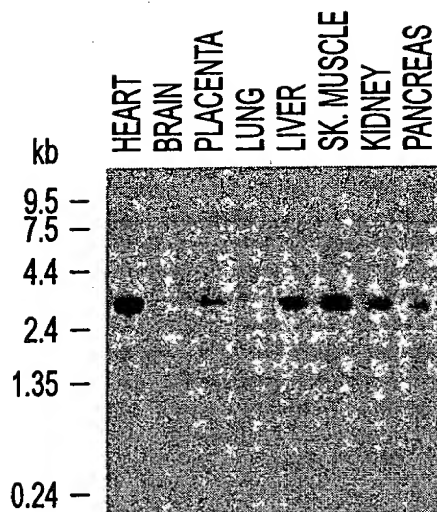


TABLE 18988660

ELAC2, N-terminal sequences		
(HSA) ELAC2	52	SGGNTVYLQVWAAGSRDGAALYVSEFNR.....YLFNCGEGVQRIM.....QEHKLKVARLDNIFLTR..MHWNVGGLSCMILTKE
(MMU) Elac2	44	PGGNTVYLQVWAAGGRDGAALYVSEYNR.....YLFNCGEGVQRIM.....QEHKLKVARLDNIFLTR..MHWNVGGLSCMILTKE
(CEL) CE16965	87	VNIPQVSIENLGN.GTGELRACFIIRTPLK.....TYMFCPENACRFL.....WQIRIRSSSVVDLFTFS..ANWDNIAGISSLLLSI.KE
(ATH) gi6850339	45	NPTNTIAYAQILGTGMDTQDTSSSVLLFEDK.....QRTEAGBGLQRFPC.....TEHKIKLSNIDHVPFSR..VCSFAGGLPELILLTAG
(SCE) YKR079C	1	MFTFPIITHTSDTKHPLLLVQSAHGEX.....YFPGKIGEGSORSL.....TENKIRISLKDIFLTGELNWSIGGLPGMILTIAID
ELAC2, His motif region		
(HSA) ELAC2	475	EKRQYPEIIFLTGSAIPNKIRNVSAATLVNISP.....DTSLLDCCGEGTFGQLCRHYGDQ.VDRVLGTAAPFVSH..LHADHTGLPSILLQREH
(MMU) Elac2	471	EKRQYPEIIFLTGSAIPNEIRNVSTLVNLSL.....DKSVLLDCGEGTFGQLCRHYGQQ.IDRVLCSTAFVESH..LHADHTGLNILLQREH
(CEL) CE16965	480	KMDCPEPKLTFEFTSSAVPSKYRNVTC.YLVEASE.....NSAILLDVGEITYGQMRVFGEDGCKQLLVNENCVLITH..AHQDENNGLYTHIARKKE
(ATH) gi6850339	479	KIRDDWEIIVILGTSSQPSKYRNVSAIFIDLS.....RGSLLDCCGEGTLGQLKRRYGLDGADEAVRKRIMISH..IHADHTGLARILALRSK
(SCE) YKR079C	460	AEKKKHVEIITLSTGSAIPSKYRNVVSTLVKVPPTDADGNTINRMIDAGENTLGTIHRNPSQLAVKSIPODKMIVLSH..LHADHTGLTISVINEWYK
ELAC1, N-terminal=His motif region		
(HSA) ELAC1	1	MSMDVIFLTGGAAYPSPTRGASAWLRCE.....GECMLFDCGEGTQTQL.....MKSQKAGRTXKIFITH..LHGDHFFGLPGLLCTISL
(Es c) elac	1	MKRDELNELIFLTGSAVPTRTRNVTA.ILLNLQHPQTQ....SGLMLFDCGEGTQHQL.....LHTAFNPGKLDKIFISH..LHGDHFFGLPGLLCQRSM
(Syn sp) gi2500943	1	MEITFLGTSSGVPTRNRNVSS.IALRLPQ.....RAELMLFDCGEGTQHQP.....LRSEWKISQTRIFITH..LHGDHFFGLMGLLASSGL
(Me t) gi2622965	1	MNEVTFLTGSSAVPSKRNHTS.IALRIP.....GEIFLFDCCGEGTORQM.....ALAGISPMXVTRIFITH..LHGDHFFGLPGMLOSMP

FIG. 12

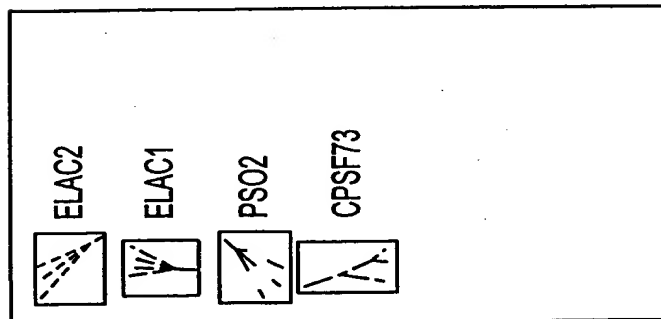


FIG. 13

Eukaryota
Eubacteria
Archaea